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FO06823: AAC51777.1; -
FO65163: AAC23340.1; -
MGNC: 6278; KCNK3.

3320: -
o: IPR003280: K+channel_2pore.
o: IPR001622: K+channel_pore.
o: IPR000636: M+channel_nlg.
o: IPR003092: TASK channel.
FO0520: Ion trans-1.
PR01333: 2PoreChannel.
PR01095: TASKChannel.
channel; Transmembrane; Ion transport; Potassium transport;
Otein.

M 1 8 CYTOPLASMIC (POTENTIAL).
M 9 29 POTENTIAL.
M 78 101 PORE-FORMING 1 (POTENTIAL).
M 108 128 POTENTIAL.
M 129 158 CYTOPLASMIC (POTENTIAL).
M 159 179 POTENTIAL.
M 184 207 PORE-FORMING 2 (POTENTIAL).
M 223 243 POTENTIAL.
M 244 354 CYTOPLASMIC (POTENTIAL).
D 33 53 N-LINKED (GLCNAC...) (POTENTIAL).
E 394 AA: 43518 MW; 9FF4C8266F615FB7 CRC64;

h 100.0%; Score 2042; DB 1; Length 394;
Similarity 100.0%; Pred. No. 1e-153;
94: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKRONVRLALIVCTFTLLVGAVALSEPELIERORLEKROELARVNLSCGYE 60
1 MKRONVRLALIVCTFTLLVGAVALSEPELIERORLEKROELARVNLSCGYE 60
1 EELRVVLRKPKKAGVOMRFAGSYFAITVITIGYGHAPSTDGKVCMEFYALGIP 120
1 EELRVVLRKPKKAGVOMRFAGSYFAITVITIGYGHAPSTDGKVCMEFYALGIP 120
1 EELRVVLRKPKKAGVOMRFAGSYFAITVITIGYGHAPSTDGKVCMEFYALGIP 120
1 TLVNFOSLGERINTLVRLYLRARAKGGMRAVDSANVNLGFFSCITLIGAAASH 180
1 TLVNFOSLGERINTLVRLYLRARAKGGMRAVDSANVNLGFFSCITLIGAAASH 180
1 TLVNFOSLGERINTLVRLYLRARAKGGMRAVDSANVNLGFFSCITLIGAAASH 180
1 YEHMTFFOAYYYCFTLLTIGFDYVALQDQALQPOVVAISFYITLGLTVGAEFLN 240
1 YEHMTFFOAYYYCFTLLTIGFDYVALQDQALQPOVVAISFYITLGLTVGAEFLN 240
1 YEHMTFFOAYYYCFTLLTIGFDYVALQDQALQPOVVAISFYITLGLTVGAEFLN 240
1 LVVLRFTMNAEDEKROAENRALLTRNGAGGGGGGSAHTTDTASTAAAGGGFRMY 300
1 LVVLRFTMNAEDEKROAENRALLTRNGAGGGGGGSAHTTDTASTAAAGGGFRMY 300
1 LVVLRFTMNAEDEKROAENRALLTRNGAGGGGGGSAHTTDTASTAAAGGGFRMY 300
1 AEVLHFOGMCSCIMYKREKLOYISIPILIPRODSTDCVEOSHSPGGGGYSPSPRR 360
1 AEVLHFOGMCSCIMYKREKLOYISIPILIPRODSTDCVEOSHSPGGGGYSPSPRR 360
1 AEVLHFOGMCSCIMYKREKLOYISIPILIPRODSTDCVEOSHSPGGGGYSPSPRR 360
1 CLCSGAPRSALSSVSTGLHSLSTRGLMKRRSSV 394
1 CLCSGAPRSALSSVSTGLHSLSTRGLMKRRSSV 394
1 CLCSGAPRSALSSVSTGLHSLSTRGLMKRRSSV 394

STANDARD: PRT: 411 AA.

2001 (Rel. 40, Created)
2001 (Rel. 40, Last sequence update)
2001 (Rel. 40, Last annotation update)
Im channel subfamily K member 3 (Acid-sensitive potassium
protein TASK) (TWIK-related acid-sensitive K+ channel).
Task.
Invertebrates (Fam).
a: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; F
OX NCBI_Taxid=10116;
RM (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=9809797; PubMed=9437008;
RA Leontidek D., Gray A.T., Winesgar B.D., Kindler C.H., Harada M
RT Taylor D.M., Chavez R.A., Forsythe J.R., Yost C.S.;
RT "An open rectifier potassium channel with two pore domains in t
J. Neurosci. 18:868-877(1998)."
CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POT
CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTAS
ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS A
OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS
WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS 1
(BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE
CC EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY A
CC SKELETAL MUSCLE.
CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, 2I
CC BUPIVACAINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASS
CC CHANNELS.
CC -----
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CC modified and this statement is not removed. Usage by and for
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF031384; AAC39952.1; -
CC InterPro: IPR003280: K+channel_2pore.
CC InterPro: IPR001622: K+channel_pore.
CC InterPro: IPR000636: M+channel_nlg.
CC InterPro: IPR003092: TASK channel.
CC Pfam: PF00520: Ion-trans-1.
CC DR PRINTS: PR01333; 2PoreChannel.
CC DR PRINTS: PR01095; TASKChannel.
CC KM Ionic channel; Transmembrane; Ion transport; Potassium transpor
CC Glycoprotein.
CC FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 9 29 POTENTIAL.
CC FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).
CC FT TRANSMEM 108 128 POTENTIAL.
CC FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 159 179 POTENTIAL.
CC FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
CC FT TRANSMEM 223 243 POTENTIAL.
CC FT DOMAIN 244 354 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SDOUCE 411 AA: 45276 MW; D2778016092B5 CRC64;

Query Match 90.6%; Score 1850.5; DB 1; Length 411;
Best Local Similarity 88.3%; Pred. No. 1.3e-138;
Matches 363; Conservative 8; Mismatches 23; Indels 17;

OY 1 MKRONVRLALIVCTFTLLVGAVALSEPELIERORLEKROELARVNLSCGYE 60
DB 1 MKRONVRLALIVCTFTLLVGAVALSEPELIERORLEKROELARVNLSCGYE 60
OY 61 EELRVVLRKPKKAGVOMRFAGSYFAITVITIGYGHAPSTDGKVCMEFYAL 120
DB 61 EELRVVLRKPKKAGVOMRFAGSYFAITVITIGYGHAPSTDGKVCMEFYAL 120
OY 121 TLVNFOSLGERINTLVRLYLRARAKGGMRAVDSANVNLGFFSCITLIGAAASH 180
DB 121 TLVNFOSLGERINTLVRLYLRARAKGGMRAVDSANVNLGFFSCITLIGAAASH 180
OY 181 YEHMTFFOAYYYCFTLLTIGFDYVALQDQALQPOVVAISFYITLGLTVGAEFLN 240
DB 181 YEHMTFFOAYYYCFTLLTIGFDYVALQDQALQPOVVAISFYITLGLTVGAEFLN 240

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)USE STANDARD; PRT; 409 AA.
)O35163;
-2001 (Rel. 40, Created)
-2001 (Rel. 40, Last sequence update)
-2001 (Rel. 40, Last annotation update)
-2001 (Rel. 40, Last annotation update)
um channel subfamily K member 3 (acid-sensitive potassium
protein TASK) [TWIK-related acid-sensitive K+ channel] .
ic two-pore background K+ channel) (citrak-1).
)R TASK OR CTBKAK.
icula (mouse).
)ta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
)a; Eutheralia; Rodentia; Sciurognathi; Muridae; Murinae; Mus
xID:-000930;

```

HE FROM N.A.
HEART;
98165556; PubMed-9506712;
Fujita A., Horio Y., Kurachi Y.;
ing and functional expression of a novel cardiac two-pore
and K⁺ channel (CTBAK-1).
kes. 82:513-518(1998).

Chem. 275:16569-16578(2000).

Leece F., Flink M., Reyes R., Heurteaux C., Lazdunski M.: A human background K⁺ channel to sense external pH variations. *Physiological pH*. 15:5464-5471 (1997)

CTION: pH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN INWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. IN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD SIMILARITY).

(UNIT: HOMODIMER (POTENTIAL)).

CELLULAR LOCATION: Integral membrane protein (potential).

SIDE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL INTESTINE, AND STOMACH. NOT DETECTED IN LIVER, THYROID OR SPLEEN.

CELLULOSES: INACTIVATED BY BARIUM.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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DR	EMBL; AB0086537.	BAA23436.1;	-
DR	EMBL; AF241198.	AAF81418.1;	-
DR	EMBL; AF242508.	AAF81418.1;	JOINED.
DR	EMBL; AF065162.	AAG29339.1;	-
DR	EMBL; AF006824.	AAC53367.1;	-
DR	EMBL; AB011345.	BAA28349.1;	-
DR	MGD; MGT1100509.	KCKK3.	
DR	Interpro; IPR003280.	K+channel_2po-	
DR	Interpro; IPR001622.	K+channel_pore.	
DR	Interpro; IPR000636.	M+channel_nlg.	
DR	Interpro; IPR003092.	TASK channel.	
DR	Pfam; PF005240.	Ion_transf. 1.	
DR	PRINTS; PR01333.	2PORECHANNEL.	
DR	PRINTS; PRO1095.	TASCKCHANNEL.	
KM	Ionic channel; Transmembrane; Ion transport; Potassium transpor		
KM	Glycoprotein.		
FT	DOMAIN	1	8
FT	TRANSMEM	9	29
FT	DOMAIN	78	101
FT	TRANSMEM	108	128
FT	DOMAIN	129	158
FT	TRANSMEM	159	179
FT	DOMAIN	184	203
FT	TRANSMEM	223	244
FT	CARBOHYD	244	409
FT	CONFLICT	53	53
FT	CONFLICT	123	4
SO	SEQUENCE	409 AA:	123 45068 MW; 35236E01AAC5687 CRC64;

Query Match	90.1%	Score 1840.5;	DB 1;	Length 409;
Best Local Similarity	88.5%;	Pred. No. 8.1e-138;		
Matches 362;	Conservative	7;	Mismatches 25;	Indels 15;

QY	1	MRQNVKRTALALVCFEYFTLLGAAVFALESPELETEROLELEKQOOLELAAARN
Db	1	MRQNVKRTALALVCFEYFTLLGAAVFALESPELETEROLELEKQOOLELAAARN
QY	61	ELEERVYLRKPKKGVQVQRFAGSFYEYATITTTTIGGHAAPSDGGKVCVMCFY
Db	61	ELEERVYLRKPKKGVQVQRFAGSFYEYATITTTTIGGHAAPSDGGKVCVMCFY
QY	121	TLVNFQSGERINELVRYLLHRANKGLGNRADVSAANVYLIGFESCISTLCIT
Db	121	TLVNFQSGERINELVRYLLHRANKGLGNRAEVSANVYLIGFESCISTLCIT
QY	181	YEHMFEPQAYYYCFITLTCTTGIGDGYALOKDOALQTPQVAFSPYILTGLT
Db	181	YEHMFEPQAYYYCFITLTCTTGIGDGYALOKDOALQTPQVAFSPYILTGLT
QY	241	LVLRFPTMNADEKRDAAERHALLFRNGQAGGGG-----GGSAMTTDTA
Db	241	LVLRFPTMNADEKRDAAERHALLFRNGQAVGGGSLGSGADVRPRDQV
QY	292	-----GGGGGRNYAAEVLNFQSSCSCTPYKSRKLOYSITPHIIPRODLSPT
Db	301	GVCVGVQSSGRNYYAAEVLNFQSSCSCTLWKKSEKQYISIPHIIPRODLSPT
QY	346	SPFGGGGRISDTPSRRCICSGAPNSAISVSTGLHSLSTRGLMKRRSSV 394
Db	361	SPFGGGGRISDTPSRPCDSCGQSRSAISVSTGLHSLTAARGLMKRRSSV 409

Water